

Effects of probiotics administration on tilapia intestinal flora and cytokine genes

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Probiotics are used frequently for prevention of an infection at tilapia aquaculture farms. It is not yet known whether the bacteria flora of the intestinal tract of a tilapia changes after administration of probiotics. The response of innate cytokine genes to administration of probiotics also have not been assessed in tilapia. Genomic DNA was extracted from the intestinal contents of cultured tilapia. The 16S rDNA V1-2 region of bacteria was amplified from the extracted DNA using the universal primers, and the amplicon was analyzed using 454 GS-FLX platform. On the basis of the bacterial 16S rDNA diversity analysis, the operational taxonomic units (OTUs) numbers were

attained from the intestinal contents of cultured tilapia. Six typical genera were observed in tilapia intestinal flora following administration with probiotics: *Clostridium*, *Cetobacterium*, *Mycobacterium*, *Bacteroides*, *Sediminibacterium* and *Nordella*. Six typical species observed in tilapia intestinal flora following administration with probiotics included: *Cellulomonas parahominis*, *Dechloromonas* sp. *MissR*, *Arthrobacter* sp. Rue61a, *Cellulomonas parahominis*, *Thioflavicoccus mobilis* and *Chthoniobacter flavus*. *Cellulomonas parahominis* was dominant in the intestinal flora of tilapia following administration probiotics. The expression of cytokine genes of IL-1beta, IL-10, IL-12, IL-17A/F, IFN-gamma and TNF-alpha of tilapia were analyzed after administration of probiotics. We will also discuss interaction in tilapia between cytokine gene expression, microbiota and probiotic administration